

AMENDMENTS

In the claims:

Please amend the claims as follows:

Please cancel claims 37-51.

1. (Original) A method for identifying a polypeptide, comprising:

(a) simultaneously determining the mass of a subset of parent polypeptides from a population of polypeptides and the mass of fragments of said subset of parent polypeptides;

(b) comparing said determined masses to a annotated polypeptide index; and

(c) identifying one or more polypeptides of said annotated polypeptide index having said determined masses.

2. (Original) The method of claim 1, further comprising:

(d) determining one or more additional characteristics associated with one or more of said parent polypeptides;

(e) comparing said characteristics determined in step (a) and step (d) to said annotated polypeptide index; and

(f) optionally repeating steps (d) and (e) one or more times, wherein a set of characteristics is determined that identifies a parent polypeptide as a single polypeptide in said annotated polypeptide index.

3. (Original) The method of claim 1, further comprising quantitating the amount of said identified polypeptide in a sample containing said polypeptide.

4. (Original) The method of claim 2, wherein a set of characteristics is determined that identifies two or more parent polypeptides as single polypeptides in said annotated polypeptide index.

5. (Original) The method of claim 4, wherein a set of characteristics is determined that identifies each of said parent polypeptides in said subset of parent polypeptides.

6. Canceled

7. (Previously amended) The method of claim 1, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of greater than 1 ppm.

8. (Previously amended) The method of claim 1, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 2.5 ppm or greater ppm.

9. (Previously amended) The method of claim 1, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 5 ppm or greater ppm.

10. (Previously amended) The method of claim 1, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 10 ppm or greater ppm.

11. (Previously amended) The method of claim 1, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 100 ppm or greater ppm.

12. (Previously amended) The method of claim 2, wherein said characteristics are selected from the group consisting of polypeptide mass, amino acid composition, isoelectric point (pI), and elution on a chromatographic medium.

13. (Previously amended) A method for identifying a polypeptide, comprising:

(a) simultaneously determining the mass of a subset of parent polypeptides from a population of polypeptides and the mass of fragments of said subset of parent polypeptides, wherein said fragment mass is determined by mass spectrometry in the absence of ion selection for producing fragment ions;

(b) comparing said determined masses to an annotated polypeptide index;

(c) identifying one or more polypeptides of said annotated polypeptide index having said determined masses; and

(d) quantitating the amount of said identified polypeptide in a sample containing said polypeptide.

14. (Original) The method of claim 13, further comprising:

(e) determining one or more additional characteristics associated with one or more of said parent polypeptides;

(f) comparing said characteristics determined in step (a) and step (e) to said annotated polypeptide index; and

(g) optionally repeating steps (e) and (f) one or more times, wherein a set of characteristics is determined that

identifies a parent polypeptide as a single polypeptide in said annotated polypeptide index.

15. (Original) The method of claim 14, wherein a set of characteristics is determined that identifies two or more parent polypeptides as single polypeptides in said annotated polypeptide index.

16. (Original) The method of claim 15, wherein a set of characteristics is determined that identifies each of said parent polypeptides in said subset of parent polypeptides.

17. Canceled.

18. (Previously amended) The method of claim 13, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of greater than 1 ppm.

19. (Previously amended) The method of claim 13, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 2.5 ppm or greater ppm.

20. (Previously amended) The method of claim 13, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 5 ppm or greater ppm.

21. (Previously amended) The method of claim 13, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 10 ppm or greater ppm.

22. (Previously amended) The method of claim 13, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 100 ppm or greater ppm.

23. (Previously amended) The method of claim 13, wherein said characteristics are selected from the group

consisting of polypeptide mass, amino acid composition, isoelectric point (pI), and elution on a chromatographic medium.

24. (Original) A method for identifying a polypeptide, comprising

(a) determining two or more characteristics associated with said polypeptide, or a fragment thereof, one of said characteristics being mass of a fragment of said polypeptide, said fragment mass being determined by mass spectrometry in the absence of ion selection for producing fragment ions;

(b) comparing said characteristics associated with said polypeptide to a polypeptide identification index; and

(c) identifying one or more polypeptides in said polypeptide identification index having said characteristics.

25. (Original) The method of claim 24, further comprising

(d) determining one or more additional characteristics associated with said polypeptide; and

(e) comparing said characteristics determined in step (a) and step (d) to said polypeptide identification index.

26. (Original) The method of claim 24, further comprising quantitating the amount of said identified polypeptide in a sample containing said polypeptide.

27. (Original) The method of claim 24, wherein said polypeptide identification index is an annotated peptide index.

28. (Original) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 1 ppm or greater ppm.

29. (Original) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 2.5 ppm or greater ppm.

30. (Original) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 5 ppm or greater ppm.

31. (Original) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 10 ppm or greater ppm.

32. (Original) The method of claim 24, wherein said fragment mass is determined at an accuracy in ppm of 100 ppm or greater ppm.

33. (Original) The method of claim 24, wherein three or more characteristics of said polypeptide are determined.

34. (Original) The method of claim 24, wherein four or more characteristics of said polypeptide are determined.

35. (Original) The method of claim 24, wherein five or more characteristics of said polypeptide are determined.

36. (Previously amended) The method of claim 24, wherein said characteristics are selected from the group consisting of polypeptide mass, amino acid composition, isoelectric point (pI), and elution on a chromatographic medium.

Claims 37-51 Canceled

52. (Original) The method of claim 36, wherein said characteristic is polypeptide mass.

53. (Original) The method of claim 36, wherein said characteristic is amino acid composition.

54. (Original) The method of claim 36, wherein said characteristic is pI.

55. (Original) The method of claim 36, wherein said characteristic is elution on a chromatographic medium.

56. (Original) A method for identifying a polypeptide, comprising:

(a) simultaneously determining the mass of a subset of parent polypeptides from a population of polypeptides and the mass of fragments of said subset of parent polypeptides, wherein said fragment mass is determined by mass spectrometry in the absence of ion selection for producing fragment ions;

(b) comparing said determined masses to a annotated polypeptide index; and

(c) identifying one or more polypeptides of said annotated polypeptide index having said determined masses.

57. (Original) The method of claim 56, further comprising:

(d) determining one or more additional characteristics associated with one or more of said parent polypeptides;

(e) comparing said characteristics determined in step (a) and step (d) to said annotated polypeptide index; and

(f) optionally repeating steps (d) and (e) one or more times, wherein a set of characteristics is determined that identifies a parent polypeptide as a single polypeptide in said annotated polypeptide index.

58. (Original) The method of claim 56, further comprising quantitating the amount of said identified polypeptide in a sample containing said polypeptide.

59. (Original) The method of claim 57, wherein a set of characteristics is determined that identifies two or more parent polypeptides as single polypeptides in said annotated polypeptide index.

60. (Original) The method of claim 59, wherein a set of characteristics is determined that identifies each of said parent polypeptides in said subset of parent polypeptides.

61. (Original) The method of claim 56, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of greater than 1 ppm.

62. (Original) The method of claim 56, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 2.5 ppm or greater ppm.

63. (Original) The method of claim 56, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 5 ppm or greater ppm.

64. (Original) The method of claim 56, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 10 ppm or greater ppm.

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65. (Original) The method of claim 56, wherein the mass of said parent polypeptides and fragments is determined at an accuracy in ppm of 100 ppm or greater ppm.

66. (Original) The method of claim 57, wherein said characteristics are selected from the group consisting of polypeptide mass, amino acid composition, pI, and elution on a chromatographic medium.

67. (Original) The method of claim 66, wherein said characteristic is polypeptide mass.

68. (Original) The method of claim 66, wherein said characteristic is amino acid composition.

69. (Original) The method of claim 66, wherein said characteristic is pI.

70. (Original) The method of claim 66, wherein said characteristic is elution on a chromatographic medium.
